

[ (see identification of Rho antagonist section).

SEQUENCE of (known) Rho antagonist C3 used in the experiments

Nucleotide sequence including part of the plasmid GST sequence. The vector with the GST sequence is commercially available and thus the entire GST sequence including the start was not sequenced. It was desired to determine only the sequence 3' to the thrombin cleavage site which releases C3 from the GST sequence. The thrombin cleavage site is shown with an arrow and is located just to the left of the underlined nucleotide sequence below (i.e. the arrow shows the thrombin cleavage site). The underlined sequence shows additional coding sequence translated in our recombinant protein that is not reported in the literature.

Both strands were sequenced to verify that there were no errors in the sequence.

↓

5' GTG GCG ACC CTT CCC AAA TCG GAT CTG GTT CCG CGT GGA TCC TCT AGA  
GTC GAC CTG CAG GCA TGC AAT GCT TAT TCC ATT AAT CAA AAG GCT TAT TCA AAT ACT TAC  
CAG GAG TTT ACT AAT ATT GAT CAA GCA AAA GCT TGG GGT AAT GCT CAG TAT AAA AAG TAT  
GGA CTA AGC AAA TCA GAA AAA GAA GCT ATA GTA TCA TAT ACT AAA AGC GCT AGT GAA ATA  
AAT GGA AAG CTA AGA CAA AAT AAG GGA GTT ATC AAT GGA TTT CCT TCA AAT TTA ATA AAA  
CAA GTT GAA CTT TTA GAT AAA TCT TTT AAT AAA ATG AAG ACC CCT GAA AAT ATT ATG TTA  
TTT AGA GGC GAC GAC CCT GCT TAT TTA GGA ACA GAA TTT CAA AAC ACT CTT CTT AAT TCA  
AAT GGT ACA ATT AAT AAA ACG GCT TTT GAA AAG GCT AAA GCT AAG TTT TTA AAT AAA GAT  
AGA CTT GAA TAT GGA TAT ATT AGT ACT TCA TTA ATG AAT GTT TCT CAA TTT GCA GGA AGA  
CCA ATT ATT ACA AAA TTT AAA GTA GCA AAA GGC TCA AAG GCA GGA TAT ATT GAC CCT ATT  
AGT GCT TTT CAG GGA CAA CTT GAA ATG TTG CTT CCT AGA CAT AGT ACT TAT CAT ATA GAC  
GAT ATG AGA TTG TCT TCT GAT GGT AAA CAA ATA ATA ATT ACA GCA ACA ATG ATG GGC ACA  
GCT ATC AAT CCT AAA TAA 3'

Nucleotide sequence of recombinant C3 protein: the sequence given below represents the entire coding sequence for the Rho antagonist used in the experiments mentioned herein. It is similar to the sequence shown above but does not include the GST portion which when the protein is made is enzymatically removed with thrombin.

1 GGATCCCTCA GAGTCGACCT GCAGGCATGC AATGCTTATT CCATTAATCA  
51 AAGGGCTTAT TCAAATACTT ACCAGGAGTT TACTAATATT GATCAAGCAA  
101 AAGCTTGGGG TAATGCTCAG TATAAAAAGT ATGGACTAAG CAAATCAGAA  
151 AAAGAAGCTA TAGTATCATA TACTAAAAGC GCTAGTGAAA TAAATGGAAA  
201 GCTAAGACAA AATAAGGGAG TTATCAGTGG ATTTCCTTCA AATTAAATAA  
251 AACAAGTTGA ACTTTAGAT AATCTTTA ATAAAATGAA GACCCCTGAA  
301 AATATTATGT TATTTAGAGG CGACGGACCT GCTTATTTAG GAACAGAATT

351 TCA~~A~~ACACT CTCTTAATT CAAATGGTAC AATTAATAAA ACGGCTTTG  
 401 AAAAGGCTA~~A~~ AGCTAAGTT TTAATAAAG ATAGACTTGA ATATGGATAT  
 451 ATTAGTACTT CATTAATGAA TGTTCTCAA TTTGCAGGAA GACCAATTAT  
 501 TACAAAATT~~A~~ AAGTAGCAA AAGGCTCAA~~A~~ GGCAGGATAT ATTGACCC~~T~~  
 551 TTAGCTCTT TCAGGGACAA CTGAAATGT TGCTTCTAG ACATAGTACT  
 601 TATCATATAG ACGATATGAG ATTGTCTTCT GATGGTAA~~C~~ AAATAATAAT  
 651 TACAGCAAC~~A~~ ATGATGGGCA CAGCTATCAA TCCTAAATAA

Amino acid sequence (one letter code)

Translation of the above sequence to show amino acid sequence. Amino acids in bold, highlight differences from published sequence (Popoff et al. (1990) Nucl. Acid. Res. 18:1291. EMBL accession no. X511464.) The 11 N-terminal sequences are additional; there is a single amino acid change of an alanine (hydrophobic) to glutamic acid (Q).

**GSSRV~~D~~LQAC** NAYSINQKAY SNTYQEFTNI DQAKAWGNAQ YKKYGLSKSE  
 KEAI~~V~~SYTKS ASEINGKLRQ NKGVINGFPS NLIKQVELLD KSFNKMKTPE NIMLF~~X~~GDDP  
 AYLGT~~E~~FQNT LLNSNGTINK TAFEKAKAKF LNXDRLEYGY ISTSLMNVSQ FAGRPIITKF  
 KVAKGSKAGY IDPISAF**Q**QQ LEMIILPRUST YHIDDMRISS DGKQHITAT MMGTA~~I~~NPK

Number of amino acids: 229

Molecular weight: 25507.5

Theoretical pI: 9.43

Amino acid composition:

Ala (A)	18	7.9%
Arg (R)	6	2.6%
Asn (N)	18	7.9%
Asp (D)	10	4.4%
Cys (C)	1	0.4%
Gln (Q)	12	5.2%
Glu (E)	10	4.4%
Gly (G)	16	7.0%
His (H)	2	0.9%
Ile (I)	18	7.9%

Leu (L)	17	7.4%
Lys (K)	23	10.0%
Met (M)	7	3.1%
Phe (F)	10	4.4%
Pro (P)	7	3.1%
Ser (S)	20	8.7%
Thr (T)	14	6.1%
Trp (W)	1	0.4%
Tyr (Y)	11	4.8%
Val (V)	6	2.6%
Asx (B)	0	0.0%
Gln (Z)	0	0.0%
Xaa (X)	2	0.9%

Total number of negatively charged residues (Asp + Glu): 20

Total number of positively charged residues (Arg + Lys): 29

Estimated half-life:

The N-terminal of the sequence considered is G (Gly).

The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).

>20 hours (yeast, in vivo).

>30 hours (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 26.88

This classifies the protein as stable.

Aliphatic index: 75.07

Grand average of hydropathicity (GRAVY): -0.479 ]

Please also delete the following passage found on pages 46 to 51;

## [ SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: LISA MCKERRACHER

(ii) TITLE OF INVENTION: Methods for making and delivering Rho-antagonist tissue adhesive formulations to the injured mammalian central and peripheral nervous systems and uses thereof

(iii) NUMBER OF SEQUENCES: 3

## (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: BROULLETTE KOSIE
- (B) STREET: 1100 RENE-LESVEQUE BLVD WEST
- (C) PROV/STATE: QUEBEC
- (D) COUNTRY: CANADA
- (E) POSTAL/ZIP CODE: H3B 5C9

## (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: ASCII (TEXT)

## (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

## (vii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: RONALD S. KOSIE
- (B) REGISTRATION NO.: 28,814
- (C) REFERENCE/DOCKET NO.: 06447-003-US-2
- (D) TEL. NO.: (514) 397 8500
- (E) FAX NO.: (514) 397 8515

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:
- (B) TYPE:
- (C) STRANDEDNESS:
- (D) TOPOLOGY:

## (ii) MOLECULE TYPE:

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (A) ORGANISM:

## (vii) IMMEDIATE SOURCE:

## (ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION:

## (x) PUBLICATION INFORMATION:

- (A) AUTHORS:
- (B) TITLE:
- (C) JOURNAL:
- (D) VOLUME:
- (E) ISSUE:
- (F) PAGES:
- (G) DATE:
- (H) DOCUMENT NO.:
- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES IN SEQ ID NO:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTG GCG ACC CTT CCC AAA TCG GAT CTG GTT CCG CGT GGA TCC TCT AGA

5 10 15  
GTC GAC CTG CAG GCA TGC AAT GCT TAT TCC ATT AAT CAA AAG GCT TAT  
20 25 30  
TCA AAT ACT TAC CAG GAG TTT ACT AAT ATT GAT CAA GCA AAA GCT TGG  
35 40 45  
GGT AAT GCT CAG TAT AAA AAG TAT GGA CTA AGC AAA TCA GAA AAA GAA  
50 55 60  
GCT ATA GTA TCA TAT ACT AAA AGC GCT AGT GAA ATA AAT GGA AAG CTA  
65 70 75 80  
AGA CAA AAT AAG GGA GTT ATC AAT GGA TTT CCT TCA AAT TTA ATA AAA  
85 90 95  
CAA GTT GAA CTT TTA GAT AAA TCT TTT AAT AAA ATG AAG ACC CCT GAA  
100 105 110  
AAT ATT ATG TTA TTT AGA GGC GAC GAC CCT GCT TAT TTA GGA ACA GAA  
115 120 125  
TTT CAA AAC ACT CTT CTT AAT TCA AAT GGT ACA ATT AAT AAA ACG GCT  
130 135 140  
TTT GAA AAG GCT AAA GCT AAG TTT TTA AAT AAA GAT AGA CTT GAA TAT  
145 150 155 160  
GGA TAT ATT AGT ACT TCA TTA ATG AAT GTT TCT CAA TTT GCA GGA AGA  
165 170 175  
CCA ATT ATT ACA AAA TTT AAA GTA GCA AAA GGC TCA AAG GCA GGA TAT  
180 185 190  
ATT GAC CCT ATT AGT GCT TTT CAG GGA CAA CTT GAA ATG TTG CTT CCT  
195 200 205  
AGA CAT AGT ACT TAT CAT ATA GAC GAT ATG AGA TTG TCT TCT GAT GGT  
210 215 220  
AAA CAA ATA ATA ATT ACA GCA ACA ATG ATG GGC ACA GCT ATC AAT CCT  
225 230 235 240  
AAA TAA

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE:

(C) STRANDEDNESS:

(D) TOPOLOGY:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(ix) FEATURE:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGATCCTCTA GAGTCGACCT GCAGGCATGC AATGCTTATT CCATTAATCA 50  
AAAGGGCTTAT TCAAAATACTT ACCAGGAGTT TACTAAATATT GATCAAGCAA 100  
AAGCTTGGGG TAATGCTCAG TATAAAAAGT ATGGACTAAG CAAATCAGAA 150  
AAAGAAGCTA TAGTATCATA TACTAAAAGC GCTAGTGAAA TAAATGGAAA 200  
GCTAAGACAA AATAAGGGAG TTATCAATGG ATTCCTTCA AATTTAATAA 250  
AACAAGTTGA ACTTTAGAT AAATCTTTA ATAAAATGAA GACCCCTGAA 300  
AATATTATGT TATTTAGAGG CGACGACCCCT GCTTATTTAG GAACAGAATT 350  
TCAAAAACACT CTTCTTAATT CAAATGGTAC AATTAATAAA ACGGCTTTG 400  
AAAGGGCTAA AGCTAAGTTT TAAATAAAG ATAGACTTGA ATATGGATAT 450  
ATTAGTACTT CATTAAATGAA TGTTCCTCAA TTTGCAGGAA GACCAATTAT 500  
TACAAAATTT AAGTAGCAA AAGGCTCAAA GGCAGGATAT ATTGACCCCTA 550  
TTAGTGCTTT TCAGGGACAA CTTGAAATGT TGCTTCCTAG ACATAGTACT 600  
TATCATATAG ACGATATGAG ATTGTCTTCT GATGGTAAAC AAATATAAT 650  
TACAGCAACAA ATGATGGGCA CAGCTATCAA TCCTAAATAA

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE:

(C) STRANDEDNESS:

(D) TOPOLOGY:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(ix) FEATURE:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GSSRVIDLQAC NAYSINQKAY SNTYQEFTNI DQAKAWGNAQ YKKYGLSKSE 50  
KEAIVSYTKS ASEINGKLQRQ NKGVINGFPS NLIKQVELLD KSFNKMKTPE 100